



6031.79428 sequence.listing.ST25
SEQUENCE LISTING

<110> Finnfeeds International, Ltd.
<120> Phytase from *Bacillus subtilis*, gene encoding said phytase, method for its production and use
<130> 79428
<140> 10/669,781
<141> 2003-09-24
<160> 36
<170> PatentIn version 3.3
<210> SEQ ID NO:1
<211> 1290
<212> DNA
<213> *Bacillus subtilis*; Strain: B13

<220>
<221> CDS
<222> (91)..(1239)

<400> 1
cacatttgac aattttcaca aaaacttaac actgacaatc atgtatataat gttacaattg 60
aagtgcacgt tcataaaaagg aggaagtaaa atg aat cat tca aaa aca ctt ttg 114
Met Asn His Ser Lys Thr Leu Leu
1 5
tta acc gcg gcg gcc gga ctg atg ctc aca tgc ggt gcg gtg tct tcc 162
Leu Thr Ala Ala Ala Gly Leu Met Leu Thr Cys Gly Ala Val Ser Ser
10 15 20
cag gca aag cat aag ctg tcc gat cct tat cat ttt acc gtg aat gca 210
Gln Ala Lys His Lys Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala
25 30 35 40
gcg gcg gaa acg gaa ccg gtt gat acg gcc ggt gac gcg gct gat gat 258
Ala Ala Glu Thr Glu Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp
45 50 55
cct gcg att tgg ctg gac ccc aag act cct cag aac agc aaa ttg att 306
Pro Ala Ile Trp Leu Asp Pro Lys Thr Pro Gln Asn Ser Lys Leu Ile
60 65 70
acg acc aat aaa aaa tca ggt tta gtc gtt tac agc ctt gat ggt aag 354
Thr Thr Asn Lys Lys Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys
75 80 85
atg ctt cat tcc tat aat acc ggg aag ctg aac aat gtc gat atc cgt 402
Met Leu His Ser Tyr Asn Thr Gly Lys Leu Asn Asn Val Asp Ile Arg
90 95 100
tat gat ttt ccg ttg aac ggc aaa aaa gtc gat atc gcg gca gca tcc 450
Tyr Asp Phe Pro Leu Asn Gly Lys Lys Val Asp Ile Ala Ala Ala Ser
105 110 115 120
aat cgg tct gaa gga aaa aat acc att gag att tac gct att gat gga 498
Asn Arg Ser Glu Gly Lys Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly

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125

130

135

546

aaa aac ggc aca tta caa agc atg aca gat cca gac cat ccg att gca
 Lys Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala
 140 145 150

594

aca gca att aat gag gta tac ggt ttt acc tta tac cac agt caa aaa
 Thr Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Tyr His Ser Gln Lys
 155 160 165

642

aca gga aaa tat tac gcg atg gtg aca gga aaa gag ggt gaa ttt gaa
 Thr Gly Lys Tyr Tyr Ala Met Val Thr Gly Lys Glu Gly Glu Phe Glu
 170 175 180

690

caa tac gaa tta aag gcg gac aaa aat gga tac ata tcc ggc aaa aag
 Gln Tyr Glu Leu Lys Ala Asp Lys Asn Gly Tyr Ile Ser Gly Lys Lys
 185 190 195 200

738

gta cgg gcg ttt aaa atg aat tcc cag acg gaa ggg atg gca gca gac
 Val Arg Ala Phe Lys Met Asn Ser Gln Thr Glu Gly Met Ala Ala Asp
 205 210 215

786

gat gaa tac ggc agg ctt tat atc gca gaa gaa gat gag gcc att tgg
 Asp Glu Tyr Gly Arg Leu Tyr Ile Ala Glu Glu Asp Glu Ala Ile Trp
 220 225 230

834

aag ttc agc gcc gag ccg gac ggc ggc agt aac gga acg gtt atc gac
 Lys Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp
 235 240 245

882

cgt gcc gac ggc agg cat tta act cgt gat att gaa gga ttg acg att
 Arg Ala Asp Gly Arg His Leu Thr Arg Asp Ile Glu Gly Leu Thr Ile
 250 255 260

930

tac tac gct gac ggg aaa ggc tat ctg atg gca tca agc cag gga
 Tyr Tyr Ala Ala Asp Gly Lys Gly Tyr Leu Met Ala Ser Ser Gln Gly
 265 270 275 280

978

aac agc agc tac gcc att tat gac aga caa gga aag aac aaa tat gtt
 Asn Ser Ser Tyr Ala Ile Tyr Asp Arg Gln Gly Lys Asn Lys Tyr Val
 285 290 295

1026

gcg gat ttt cgc ata aca gac ggt cct gaa aca gac ggg aca agc gat
 Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr Ser Asp
 300 305 310

1074

aca gac gga att gac gtt ctg ggt ttc gga ctg ggg cct gaa tat ccg
 Thr Asp Gly Ile Asp Val Leu Gly Phe Gly Leu Gly Pro Glu Tyr Pro
 315 320 325

1122

ttc ggt att ttt gtc gca cag gac ggt gaa aat ata gat cac ggc caa
 Phe Gly Ile Phe Val Ala Gln Asp Gly Glu Asn Ile Asp His Gly Gln
 330 335 340

1170

aag gcc aat caa aat ttt aaa atc gtg cca tgg gaa aga att gct gat
 Lys Ala Asn Gln Asn Phe Lys Ile Val Pro Trp Glu Arg Ile Ala Asp
 345 350 355 360

1218

caa atc ggt ttc cgc ccg ctg gca aat gaa cag gtt gac ccg aga aaa
 Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp Pro Arg Lys
 365 370 375

1269

ctg acc gac aga agc gga aaa taaacatgca aaaagcagct tataacaagct

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Leu Thr Asp Arg Ser Gly Lys
380

gcttttgca tgtgaagaac g 1290

<210> SEQ ID NO:2

<211> 383

<212> PRT

<213> *Bacillus subtilis*; Strain: B13

<400> 2

Met Asn His Ser Lys Thr Leu Leu Leu Thr Ala Ala Ala Gly Leu Met
1 5 10 15

Leu Thr Cys Gly Ala Val Ser Ser Gln Ala Lys His Lys Leu Ser Asp
20 25 30

Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu Pro Val Asp
35 40 45

Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Trp Leu Asp Pro Lys
50 55 60

Thr Pro Gln Asn Ser Lys Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu
65 70 75 80

Val Val Tyr Ser Leu Asp Gly Lys Met Leu His Ser Tyr Asn Thr Gly
85 90 95

Lys Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
100 105 110

Lys Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys Asn Thr
115 120 125

Ile Glu Ile Tyr Ala Ile Asp Gly Lys Asn Gly Thr Leu Gln Ser Met
130 135 140

Thr Asp Pro Asp His Pro Ile Ala Thr Ala Ile Asn Glu Val Tyr Gly
145 150 155 160

Phe Thr Leu Tyr His Ser Gln Lys Thr Gly Lys Tyr Tyr Ala Met Val
165 170 175

Thr Gly Lys Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys Ala Asp Lys
180 185 190

Asn Gly Tyr Ile Ser Gly Lys Lys Val Arg Ala Phe Lys Met Asn Ser
195 200 205

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Gln Thr Glu Gly Met Ala Ala Asp Asp Glu Tyr Gly Arg Leu Tyr Ile
210 215 220

Ala Glu Glu Asp Glu Ala Ile Trp Lys Phe Ser Ala Glu Pro Asp Gly
225 230 235 240

Gly Ser Asn Gly Thr Val Ile Asp Arg Ala Asp Gly Arg His Leu Thr
245 250 255

Arg Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Ala Ala Asp Gly Lys Gly
260 265 270

Tyr Leu Met Ala Ser Ser Gln Gly Asn Ser Ser Tyr Ala Ile Tyr Asp
275 280 285

Arg Gln Gly Lys Asn Lys Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly
290 295 300

Pro Glu Thr Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Leu Gly
305 310 315 320

Phe Gly Leu Gly Pro Glu Tyr Pro Phe Gly Ile Phe Val Ala Gln Asp
325 330 335

Gly Glu Asn Ile Asp His Gly Gln Lys Ala Asn Gln Asn Phe Lys Ile
340 345 350

Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala
355 360 365

Asn Glu Gln Val Asp Pro Arg Lys Leu Thr Asp Arg Ser Gly Lys
370 375 380

<210> SEQ ID NO:3
<211> 25
<212> PRT
<213> *Bacillus subtilis*

<400> 3

Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
1 5 10 15

Pro Val Asp Thr Ala Gly Asp Ala Ala
20 25

<210> SEQ ID NO:4
<211> 32

6031.79428 sequence.listing.ST25

<212> PRT

<213> Bacillus subtilis

<400> 4

Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
1 5 10 15

Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Leu Asp
20 25 30

<210> SEQ ID NO:5

<211> 8

<212> PRT

<213> Bacillus subtilis

<400> 5

Tyr Tyr Ala Met Val Thr Gly Lys
1 5

<210> SEQ ID NO:6

<211> 10

<212> PRT

<213> Bacillus subtilis

<400> 6

Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys
1 5 10

<210> SEQ ID NO:7

<211> 9

<212> PRT

<213> Bacillus subtilis

<400> 7

Met Leu His Ser Tyr Asn Thr Gly Lys
1 5

<210> SEQ ID NO:8

<211> 6

<212> PRT

<213> Bacillus subtilis

<400> 8

Ile Val Pro Trp Glu Arg
1 5

<210> SEQ ID NO:9

<211> 25

<212> PRT

<213> Bacillus subtilis

<400> 9

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Ile Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu
1 5 10 15

Ala Asn Glu Gln Val Asp Pro Arg Lys
20 25

<210> SEQ ID NO:10

<211> 30

<212> PRT

<213> *Bacillus subtilis*

<400> 10

Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala Thr
1 5 10 15

Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Trp His Ser Gln
20 25 30

<210> SEQ ID NO:11

<211> 23

<212> PRT

<213> *Bacillus subtilis*

<400> 11

Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr
1 5 10 15

Ser Asp Asp Asp Gly Ile Ile
20

<210> SEQ ID NO:12

<211> 7

<212> PRT

<213> *Bacillus subtilis*

<400> 12

Leu Thr Asp Arg Ser Gly Lys
1 5

<210> SEQ ID NO:13

<211> 13

<212> PRT

<213> *Bacillus subtilis*

<400> 13

Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys
1 5 10

<210> SEQ ID NO:14

<211> 19

6031.79428 sequence.listing.ST25

<212> PRT

<213> Bacillus subtilis

<400> 14

Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp
1 5 10 15

Pro Arg Lys

<210> SEQ ID NO:15

<211> 6

<212> PRT

<213> Bacillus subtilis

<400> 15

Ala Asn Gln Asn Phe Lys
1 5

<210> SEQ ID NO:16

<211> 5

<212> PRT

<213> Bacillus subtilis

<400> 16

Val Arg Ala Phe Lys
1 5

<210> SEQ ID NO:17

<211> 11

<212> PRT

<213> Bacillus subtilis

<400> 17

Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro
1 5 10

<210> SEQ ID NO:18

<211> 15

<212> PRT

<213> Bacillus subtilis

<400> 18

Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
1 5 10 15

<210> SEQ ID NO:19

<211> 11

<212> PRT

<213> Bacillus subtilis

<400> 19

6031.79428 sequence.listing.ST25

Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly Lys
1 5 10

<210> SEQ ID NO:20

<211> 11

<212> PRT

<213> *Bacillus subtilis*

<400> 20

Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys
1 5 10

<210> SEQ ID NO:21

<211> 22

<212> PRT

<213> *Bacillus subtilis*

<400> 21

Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp Arg
1 5 10 15

Ala Asp Gly Arg His Leu
20

<210> SEQ ID NO:22

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Synthesized

<220>

<221> modified_base

<222> (1)..(23)

<223> All Ns represents inosine

<400> 22

tcngatccnt atcattttac ngt

23

<210> SEQ ID NO:23

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Synthesized

<220>

<221> modified_base

<222> (1)..(23)

<223> N represents inosine

6031.79428 sequence.listing.ST25

<400> 23
agmggaaaat catancyrat atc 23

<210> SEQ ID NO:24
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base
<222> (1)..(22)
<223> All N's represent inosine

<400> 24
cttcnganck rttnangcn gc 22

<210> SEQ ID NO:25
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base
<222> (1)..(20)
<223> All N's represent inosine

<400> 25
tgatcngcra tnckttccca 20

<210> SEQ ID NO:26
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<400> 26
gcratmggat gatcmggatc 20

<210> SEQ ID NO:27
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base

6031.79428 sequence.listing.ST25

<222> (1)..(21)
<223> N represents inosine

<400> 27
ttccataytgt tcaaattcnc c

21

<210> SEQ ID NO:28
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base
<222> (1)..(26)
<223> All N's represent inosine

<400> 28
ttncncngtrt tatangaatg narcat

26

<210> SEQ ID NO:29
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base
<222> (1)..(20)
<223> N represents inosine

<400> 29
ccatcratng cataratttc

20

<210> SEQ ID NO:30
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> modified_base
<222> (1)..(18)
<223> N represents inosine

<400> 30
tttaaarttgy tgrrttngc

18

<210> SEQ ID NO:31

6031.79428 sequence.listing.ST25

<211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> Synthesized

<220>
 <221> modified_base
 <222> (1)..(18)
 <223> All N's represent inosine

<400> 31
 tttncncngtn accatngc

18

<210> SEQ ID NO:32
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> Synthesized

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> n is a, c, g, or t

<400> 32
 gayccdtayc ayttyacdgt naaygcgacd gcdgaaac

38

<210> SEQ ID NO:33
 <211> 52
 <212> DNA
 <213> Artificial

<220>
 <223> Synthesized

<220>
 <221> misc_feature
 <222> (7)..(14)
 <223> Mfe I site

<220>
 <221> RBS
 <222> (14)..(19)

<220>
 <221> CDS
 <222> (27)..(50)

<400> 33
 gtttctcaat tgaaggagga atttaa atg ctg tcc gat cct tat cat ttt ac
 Met Leu Ser Asp Pro Tyr His Phe

1

5

52

6031.79428 sequence.listing.ST25

<210> SEQ ID NO:34
<211> 8
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34

Met Leu Ser Asp Pro Tyr His Phe
1 5

<210> SEQ ID NO:35
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> misc_feature
<222> (6)..(11)
<223> Sal I site

<400> 35
aataagtcga cgtacgaccc gattccggct gtgct 35

<210> SEQ ID NO:36
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Synthesized

<220>
<221> misc_feature
<222> (6)..(11)
<223> Bgl II site

<400> 36
aataaagatc ttttccgct tctgtcggtc agtt 34